REMARKS

Claims 113-120, 123-125, 127-135, 149, 150 and 196-213 are pending in the application. Claims 207-211 have been amended. New claims 214-224 have been added. Accordingly, claims 113-120, 123-125, 127-135, 149, 150 and 196-224 are pending following entry of the above amendments.

No new matter has been added. For the Examiner's convenience, the claims that will be pending in the application upon entry of the instant Amendment are set forth in Appendix A.

Any amendments to and/or cancellation of the claims is not to be construed as an acquiescence to any of the rejections set forth in the instant Office Action, and was done solely to expedite prosecution of the application. Applicant hereby reserves the right to pursue the subject matter of the claims as originally filed in this or a separate application(s).

Claim Rejections - 35 USC § 101 and §112

Claims 113-120, 123-125, 127-135, 149-150 and 196-213 are rejected under 35 U.S.C. §101 because, according to the Examiner, "the claimed invention is not supported by either a specific and substantial, a credible asserted utility or a well established utility." In particular, it is the Examiner's position that

> "[w]hile applicant asserts specific utilities for the claimed invention (use of the polypeptide to treat Helicobacter pylori infection and to stimulate an immune response, these are not considered to be substantial utilities for the following reasons. These utilities are premised on the antigenicity of the polypeptide (SEQ ID NO 764) isolated from Helicobacter pylori but claims polypeptides that are cross reactive with other polypeptides and shares from 60 % sequence identity with SEQ ID NO 764 and claims polypeptides with, from 10 amino acids of SEQ ID No 764. No single functional characteristic of SEQ ID NO 764 is ascribed to the claimed polypeptide other than antigenicity."

Claims 113-120, 123-125, 127-135, 149-150 and 196-213 also stand rejected under 35 U.S.C. §112, first paragraph, because, according to the Examiner, "since the claimed invention is not supported by either a specific and substantial, a credible asserted utility or a well established

utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention." Applicant respectfully traverses this rejection.

The pending claims are drawn to isolated polypeptides comprising the amino acid sequence of SEQ ID NO: 764 and fragments thereof, *e.g.*, polypeptides comprising at least 10 consecutive amino acid residues of SEQ ID NO:764; isolated polypeptides comprising an amino acid sequence of a naturally occurring *H. pylori* polypeptide having at least 60% identity with the polypeptide set forth as SEQ ID NO: 764, or which are encoded by a nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleotide sequence encoding the polypeptide set forth as SEQ ID NO: 764; and isolated polypeptides comprising at least one epitope recognized by a T cell receptor specific for the polypeptide set forth as SEQ ID NO: 764, at least one antigenic determinant of the polypeptide set forth as SEQ ID NO: 764, or which are immunologically crossreactive with the polypeptide set forth as SEQ ID NO: 764.

The present invention features a novel surface protein from the bacteria *Helicobacter pylori*. Applicant has described the chemical, physical, and biological properties of the polypeptide set forth as SEQ ID NO: 764. Applicant asserts that the polypeptides of the invention can be used for diagnostic and therapeutic purposes with regard to *H. pylori* infection; for generating antibodies; and to evaluate compounds useful as activators or inhibitors of the bacterial life cycle (see, for example, the specification at page 50). Applicant maintains that the proposed utilities are specific and substantial utilities that satisfy the requirements of 35 U.S.C. § 101.

The specificity of the asserted utilities is based on the fact that the polypeptide set forth as SEQ ID NO: 764 is a surface protein of the *H. pylori* pathogen, and, as such, is an attractive target for intervention. The significant pathologies attributed to *H. pylori* infection (*e.g.*, gastritis, peptic ulceration, gastric cancer) have made effective diagnosis, treatment and prevention desirable. Accordingly, Applicant asserts that the claimed polypeptides possess a specific and credible utility, as all polypeptides are not capable of utility for diagnostics and therapeutics for *H. pylori*.

As support of Applicant's specific proposed utilities of the claimed polypeptides, Applicant draws the Examiner attention to the fact that *H. pylori* bacterial surface polypeptides having structural and functional homology to the polypeptide set forth as SEQ ID NO: 764 have

been reported as being important in the diagnosis and therapy of *H. pylori* infection (see, *e.g.*, Doig, P *et al.* (1995) J. Bacteriology 177:5447, and Bina J *et al.* (2000) J. Bacteriology 182:2370, copies of which are included herewith as Appendices B and C, respectively). Each of these publications describes members of the HOP family of molecules, bacterial porin proteins which are know to share chemical, physical and biological properties. These bacterial porin proteins are proposed to play a role in modulating the susceptibility of bacteria to antimicrobial therapy by influencing the permeability of the bacterial membrane, as well as a role in pathogenesis, *e.g.*, immunobiological activities in modifying the behavior of polymorphonuclear leukocytes and inducing the release of cytokines from human lymphocytes-monocytes. In fact, as described by Bina *et al.*, a member of this family, HopE (to which SEQ ID NO:764 corresponds substantially), has been shown to be antigenic *in vivo* as assessed by sera taken from *H. pylori*-infected individuals, and is immunologically conserved with both patient sera and specific monoclonal antibodies. The above-cited references provide extrinsic evidence of the asserted utility of the presently claimed polypeptides as useful for diagnostic and therapeutic purposes with regard to *H. pylori* infection; for generating antibodies; and to evaluate compounds useful as activators or inhibitors of the bacterial life cycle. In addition, porins, including the P2 porin of *H. influenzae,* have been used as immunogens that are actively and/or passively protective in subsequent challenge experiments (see, for example, Doig *et al.* at page 5451, left column, last full paragraph).

Moreover, the utilities asserted by Applicant are not "throw away" utilities (*e.g.*, use as a food supplement or cosmetic additive). As the Examiner is aware, an applicant must provide only one credible assertion of specific utility for any claimed invention to satisfy the utility requirement. The instant application teaches a specific and significant role for the claimed polypeptides. No evidence has been made of record that Applicant's assertions regarding utilities of the claimed polypeptides as diagnostic and/or therapeutic agents for *H. pylori* infection would not be considered credible to one of skill in the art. Moreover, it is Applicant's position that the Examiner's statements of record fail to constitute a reasoned explanation as to why the utilities asserted by Applicant would not be specific and substantial. Accordingly, Applicant respectfully requests reconsideration and withdrawal of this rejection.

Claim Rejections - 35 USC § 112

Rejection of Claims 113-120, 123 and 125-141 Under 35 U.S.C. §112, First Paragraph

The Examiner has maintained the rejection of claims 113-120, 123 and 125-141 under 35 U.S.C. §112, first paragraph, "as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention" for the reasons of record (Paper No. 26). Specifically, the Examiner is of the opinion that

> [a]s the instant specification is clearly enabled and provides written descriptive support for SEQ ID No 764, no specific isolated or recombinant polypeptides which share 60%,70%,80%,90%,95%,98% or 99% sequence identity evidence original descriptive support in the instant specification.

The Examiner further argues that

> [c]ompositions comprising specific immunogenic polypeptides which comprise any 5-100 consecutive amino acids are not taught in such a way as to define an effective amount of immunogenic polypeptide as the administration of SEQ ID NO 764 does not evidence original descriptive support in the instant specification. The claimed immunogenic polypeptides do not consist of SEQ ID No 764 but portions of the SEQ ID are included in a larger immunogenic polypeptide as now claimed. No specific immunogenic polypeptide, which are not immunogenic fragments of the recited SEQ ID NO 764, are described. The portions of SEQ ID NO 764 which are used in the formulation of the claimed immunogenic polypeptides need not be immunogen portions of SEQ ID No 764.

Claims 126 and 136-141 are no longer pending in the instant application having been cancelled in Applicant's amendment of January 31, 2000. With regard to claims 113-120, 123, 125, and 127-135, Applicant respectfully traverses the aforementioned rejection for the reasons set forth in Applicant's Amendment of January 31, 2000, the substance of which is reiterated here.

I. The Specification Provides Sufficient Written Description Of Polypeptides Having At Least 60% Sequence Identity With SEQ ID NO:764

With regard to the Examiner's assertion that isolated polypeptides which share 60-99% sequence identity with SEQ ID NO:764 do not evidence original descriptive support in the specification, Applicant respectfully submits that there is sufficient written description in the instant specification to inform a skilled artisan that Applicant was in possession of the claimed invention at the time of filing, as required by U.S.C. §112, first paragraph (see M.P.E.P. 2163.02).

"Written description may be satisfied through disclosure of relevant identifying characteristics, i.e., structure, other physical and/or chemical characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics." *Interim Guidelines for Examination of Patent Applications Under the 35 U.S.C. §112, First Paragraph Written Description Requirement.* Moreover, "[a] specification may, within the meaning of 35 U.S.C., § 112, First Paragraph, contain a written description of a broadly written claimed invention without describing all species that claim encompasses." *Utter v. Hiraga*, 845 F.2d 993, 6 USPQ2d 1709 (Fed. Cir. 1988). For at least the reasons discussed below, the instant specification satisfies this requirement for the claimed invention.

Claim 113 is directed to an isolated polypeptide comprising an amino acid sequence that is identical to an amino acid sequence of a ***naturally occurring*** *H. pylori* polypeptide which has at least 60% sequence identity with SEQ ID NO:764. Claims 114-119 depend from and further limit claim 113 by specifying that the polypeptide comprises at least 70%, 80%, 90%, 95%, 98% and 99% sequence identity with SEQ ID NO:764, respectively. Claims 132 and 133 depend from claim 113.

Claim 120 is directed to an isolated polypeptide comprising an amino acid sequence that is identical to an amino acid sequence of a ***naturally occurring*** *H. pylori* polypeptide, the polypeptide comprising at least 10 amino acids and being encoded by a nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleotide sequence encoding SEQ ID NO:764. Claims 132 and 133 depend from claim 120.

Claim 123 is directed to isolated, recombinant polypeptides which comprise at least one ***epitope recognized by a T cell receptor*** specific for the polypeptide set forth in SEQ ID NO: 764; which comprise at least one ***antigenic determinant*** of the polypeptide set forth in SEQ ID NO: 764; and which are ***immunologically crossreactive*** with the polypeptide set forth in SEQ ID NO:764, as recited in claims 196-204.

Applicant respectfully submits that the claimed genus of polypeptides having at least 60% sequence identity with SEQ ID NO:764 and polypeptides encoded by a nucleic acid sequence which hybridizes under high stringency conditions to the complement of a nucleotide sequence encoding SEQ ID NO:764 is defined by *structural* and *functional* features that are described in the specification, recited in the claims, and commonly possessed by its members. Firstly, the specification teaches the structure, *e.g.*, the amino acid sequence of a polypeptide (SEQ ID NO:764), common to each of the claimed polypeptides. The specification further teaches at, for example, page 50, lines 24 through page 51, line 2, and at page 72, lines 25-31 that the invention includes allelic variations, as well as natural and induced mutants of the polypeptides of the invention. In addition, the instant specification describes in detail how to make the claimed polypeptides (see, for example, pages 58-60 and pages 64-67), how to assay for functional activity, *e.g.*, immunogenecity (see, for example, pages 60-61), and how to use the polypeptides (see, for example, pages 56-58). Thus, the teachings of the instant specification convey that Applicant was in possession of the claimed invention and had a full conception of the scope of the invention at the time the application was filed.

Furthermore, claims 113 and 120, are drawn to isolated polypeptides which include an amino acid sequence that is identical to a ***naturally occurring*** *H. pylori* polypeptide. Applicant teaches that such naturally occurring polypeptides can be identified by determining sequence identity with the amino acid sequence of SEQ ID NO:764 or by detecting hybridization of the nucleic acid encoding the polypeptide with a complement of the nucleic acid sequence encoding SEQ ID NO:764 under high stringency conditions. In view of the above remarks, Applicant respectfully requests that the Examiner reconsider and withdraw this rejection.

II. The Specification Provides Sufficient Written Description Of Compositions Comprising Immunogenic Polypeptides Comprising At Least 10 Consecutive Amino Acids

With regard to the Examiner's assertion that immunogenic fragments of the polypeptide of SEQ ID NO:764 do not evidence original descriptive support in the specification, Applicant respectfully submits that there is sufficient written description in the instant specification to inform a skilled artisan that Applicant was in possession of the claimed invention at the time of filing.

Claim 125 is directed to an isolated polypeptide comprising at least 10 consecutive amino acid residues of SEQ ID NO:764. Claims 127-131 depend from and further limit claim 125 by specifying that the isolated polypeptide comprises at least about 12, 16, 20, 50 and 100 consecutive amino acid residues, respectively, of SEQ ID NO:764. Claims 134 and 135 depend from claim 125.

The Examiner has taken the position that compositions comprising specific immunogenic polypeptides are not taught in such a way as to define an effective amount of the immunogenic polypeptide. Applicant respectfully submits that claim 125 does not recite the term "immunogenic" and thus as applied to this claim and claims which depend therefrom, the above-quoted rejection is rendered moot.

However, with regard to claims 202-204 which recite isolated polypeptides comprising at least 10 consecutive amino acid residues of SEQ ID NO:764 and having at least one epitope recognized by a T cell receptor specific for the polypeptide set forth in SEQ ID NO:764; at least one antigenic determinant of the polypeptide set forth in SEQ ID NO:764; or which is immunologically crossreactive with the polypeptide set forth in SEQ ID NO:764, Applicant reiterates the following remarks of record.

Applicant's specification defines an immunogenic polypeptide as having the ability to induce a T cell response such as stimulation (*e.g.*, proliferation, cytokine secretion). In particular, an immunogenic polypeptide which has the ability to stimulate T cells is defined as comprising at least one T cell epitope which can stimulate a T cell population with the relevant T cell receptor for the epitope (see, for example, the specification at pages 60-61). In addition, an immunogenic polypeptide is described as comprising an antigenic determinant which is

specifically recognized by antibodies that recognize that polypeptide (see, for example, the specification at page 57). These structural and functional characteristics of immunogenic polypeptides are recited in claims 202-204.

Applicant respectfully submits that the common features of the immunogenic fragments of the polypeptide of SEQ ID NO:764 are taught in the specification and recited in the claims. For example, the instant specification describes in detail how to enhance the immunogenecity of the claimed polypeptides (see, for example, pages 57-59), how to identify immunogenic polypeptides *in vitro* based on the ability to induce a T cell response (see, for example, pages 60-61), and how to use the polypeptides, *e.g.*, to generate antibodies (see, for example, pages 56-58).

In view of the above, Applicant respectfully submits that pending claims are meet the written description provisions of 35 U.S.C. §112, first paragraph. Accordingly, Applicant respectfully requests reconsideration and withdrawal of this rejection.

Rejection of Claims 113-120, 123, 125, 127-135,149, 150 and 196-213 Under 35 U.S.C. §112, First Paragraph

The Examiner has also rejected claims 113-120, 123, 125, 127-135,149, 150 and 196-213 under 35 U.S.C. §112, first paragraph, "as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention." In particular, the Examiner alleges that

> "[t]he specification does not provide written description support for any flanking nucleic acid sequences which are 5' or 3' of the polynucleotide that encodes a polypeptide of SEQ ID NO:764. With the exception of an isolated polypetide that is encoded by a polynucleotide consisting of SEQ ID NO:764. The skilled artisan cannot envision all the contemplated nucleotide sequences by the detailed chemical structure of the claimed polynucleotides and therefore conception cannot be not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. "

The Examiner concludes that, "[i]n the instant case the specification provides only written description for a polypeptide that is encoded by a polynucleotide consisting of SEQ ID NO:764." Applicant respectfully traverses.

Applicant respectfully submits that the pending claimed are directed to isolated ***polypeptides*** comprising SEQ ID NO: 764 and fragments thereof, as well as isolated ***polypeptides*** comprising an amino acid sequence of a naturally occurring *H. pylori* polypeptide having at least 60% identity with the polypeptide set forth as SEQ ID NO: 764, or which are encoded by a nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleotide sequence encoding the polypeptide set forth as SEQ ID NO: 764, and isolated ***polypeptides*** comprising at least one epitope recognized by a T cell receptor specific for the polypeptide set forth as SEQ ID NO: 764, at least one antigenic determinant of the polypeptide set forth as SEQ ID NO: 764, or which are immunologically crossreactive with the polypeptide set forth as SEQ ID NO: 764.

As discussed above, the instant specification provides an adequate description of a genus encompassing a variety of species of naturally occurring *H. pylori* polypeptides and polypeptides comprising antigenic determinants of the polypeptide set forth as SEQ ID NO:764. Accordingly, Applicant respectfully requests reconsideration and withdrawal of this rejection.

Claim Rejections - 35 USC § 102

The Examiner has maintained the rejection of claims 120-123, 132-135, 149, 152 and 155 under 35 U.S.C. §102(b) as being anticipated by Newman *et al.* (1994) for the reasons of record (Paper No. 26). In particular, the Examiner characterizes the Newman *et al.* reference as follows

> Newman *et al* disclose a nucleotide sequence which encodes an isolated or purified recombinant polypeptide wherein the nucleic acid sequence share 76.923 sequence similarity and would hybridize under stringent conditions to SEQ ID No 764 and therefore anticipates the now claimed polypeptide.

Applicant respectfully traverses this rejection. Claims 121, 122, 152 and 155 are no longer pending in the instant application having been cancelled in Applicant's amendment of January 31, 2000. Moreover, claims 120, 123, 132-135 and 149 are not anticipated by the art cited for the reasons set forth in Applicant's Amendment of January 31, 2000, the substance of which is reiterated here.

For a prior art reference to anticipate a claimed invention in terms of 35 USC § 102, the prior art must teach ***each and every element*** of the claimed invention. Lewmar Marine v. Barient, 827 F.2d 744, 3 USPQ2d 1766 (Fed. Cir. 1987).

Claim 120 is directed to an isolated polypeptide comprising an amino acid sequence that is identical to an amino acid sequence of a ***naturally occurring*** *H. pylori* polypeptide, the polypeptide comprising at least 10 amino acid residues and being encoded by a nucleotide sequence that hybridizes under highly stringent conditions to the complement of a nucleotide sequence encoding SEQ ID NO:764. Claim 123 is directed to isolated, recombinant polypeptides which comprise at least one epitope recognized by a T cell receptor specific for the polypeptide set forth in SEQ ID NO: 764; which comprise at least one antigenic determinant of the polypeptide set forth in SEQ ID NO: 764; and which are immunologically crossreactive with the polypeptide set forth in SEQ ID NO:764, as recited in claims 196-204. Claims 132-135 are directed to fusion proteins comprising a polypeptide of any one of claims 113, 120, 125 or 196-204 and an additional amino acid sequence, *e.g.*, an *H. pylori* polypeptide. Claim 149 is drawn to a composition comprising a polypeptide of any one of claims 113, 120, or 196-204.

Newman *et al.* disclose the partial sequencing of anonymous ***Arabidopsis*** cDNA clones. The Examiner has cited a 75 base pair nucleic acid fragment within a cDNA clone of Newman *et al.* that, when translated in the *reverse* orientation from the *complementary* strand, encodes a ***polypeptide*** that is 42.3% *identical* and 76.9% *similar* to a polypeptide fragment of SEQ ID NO:764. Newman *et al.* does not translate in the reverse orientation the 75 nucleotides as suggested by the Examiner. Moreover, a nucleotide sequence that is complementary to a cDNA sequence (*e.g.*, a cDNA sequence comprising an open reading frame encoding a polypeptide) is not transcribed and translated in a cell, and would not be expected to encode a functional polypeptide.

Thus, Applicant respectfully submits that the cDNA of Newman *et al.* fails to teach or suggest an isolated polypeptide comprising an amino acid sequence that is identical to an amino acid sequence of a naturally occurring *H. pylori* polypeptide, as is required by claim 120. In addition, Applicant respectfully submits that it is unknown whether the cDNA fragment of Newman *et al.* would hybridize to the complement of a nucleotide sequence encoding SEQ ID NO:764 under high stringency conditions, as the sequence alignment provided by the Examiner

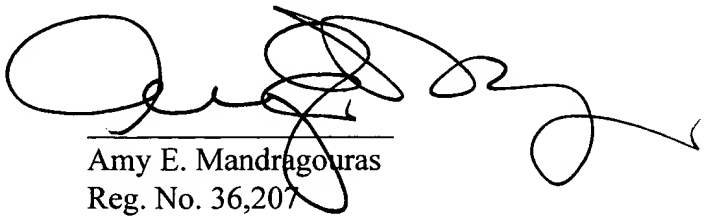
does not allow a quantitative assessment of the degree of nucleotide sequence similarity between the nucleotide sequence of Newman *et al.* and the complement of the nucleotide sequence encoding SEQ ID NO:764. Furthermore, Newman *et al.* fails to teach or suggest recombinant polypeptides which comprise at least one epitope recognized by a T cell receptor specific for the polypeptide set forth in SEQ ID NO: 764; at least one antigenic determinant of the polypeptide set forth in SEQ ID NO: 764; and which are immunologically crossreactive with the polypeptide set forth in SEQ ID NO:764 , as is required by claim 123.

Accordingly, Applicant respectfully requests reconsideration and withdrawal of this rejection.

CONCLUSION

In view of the foregoing amendments and remarks, reconsideration of the rejections and allowance of all pending claims are respectfully requested. If a telephone conversation with Applicant's Attorney would expedite prosecution of the above-identified application, the Examiner is urged to call the undersigned at (617) 227-7400.

Respectfully submitted,



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APPENDIX A

113. An isolated polypeptide comprising an amino acid sequence that is identical to an amino acid sequence of a naturally occurring *H. pylori* polypeptide, wherein said isolated polypeptide has at least 60 percent sequence identity with SEQ ID NO: 764.

114. The isolated polypeptide of claim 113 comprising an amino acid sequence having at least 70 percent sequence identity with SEQ ID NO: 764.

115. The isolated polypeptide of claim 113 comprising an amino acid sequence having at least 80 percent sequence identity with SEQ ID NO: 764.

116. The isolated polypeptide of claim 113 comprising an amino acid sequence having at least 90 percent sequence identity with SEQ ID NO: 764.

117. The isolated polypeptide of claim 113 comprising an amino acid sequence having at least 95 percent sequence identity with SEQ ID NO: 764.

118. The isolated polypeptide of claim 113 comprising an amino acid sequence having at least 98 percent sequence identity with SEQ ID NO: 764.

119. The isolated polypeptide of claim 113 comprising an amino acid sequence having at least 99 percent sequence identity with SEQ ID NO: 764.

120. An isolated polypeptide comprising an amino acid sequence that is identical to an amino acid sequence of a naturally occurring *H. pylori* polypeptide, wherein said isolated polypeptide comprises at least 10 amino acid residues and is encoded by a nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleotide sequence encoding SEQ ID NO: 764.

123. An isolated polypeptide of any one of claims 196-204 which is a recombinant polypeptide.

124. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 764.

125. An isolated polypeptide comprising at least 10 consecutive amino acid residues of SEQ ID NO: 764.

127. The isolated polypeptide of claim 125 comprising at least about 12 consecutive amino acid residues of SEQ ID NO: 764.

128. The isolated polypeptide of claim 125 comprising at least about 16 consecutive amino acid residues of SEQ ID NO: 764.

129. The isolated polypeptide of claim 125 comprising at least about 20 consecutive amino acid residues of SEQ ID NO: 764.

130. The isolated polypeptide of claim 125 comprising at least about 50 consecutive amino acid residues of SEQ ID NO: 764.

131. The isolated polypeptide of claim 125 comprising at least about 100 consecutive amino acid residues of SEQ ID NO: 764.

132. A fusion protein comprising a polypeptide of any one of claims 113, 120 or 196-204 and an additional amino acid sequence.

133. The fusion protein of claim 132, wherein the additional amino acid sequence comprises an *H. pylori* polypeptide.

134. A fusion protein comprising a polypeptide of claim 125 and an additional amino acid sequence.

135. The fusion protein of claim 134, wherein the additional amino acid sequence comprises an *H. pylori* polypeptide.

149. A composition comprising a polypeptide of any one of claims 113, 120 or 196-204 and a pharmaceutically acceptable carrier.

150. A composition comprising a polypeptide of claim 125 and a pharmaceutically acceptable carrier.

196. An isolated polypeptide comprising at least one epitope recognized by a T cell receptor specific for the polypeptide set forth in SEQ ID NO:764, said isolated polypeptide comprising an amino acid sequence having at least 60 percent sequence identity with SEQ ID NO: 764.

197. An isolated polypeptide comprising at least one antigenic determinant of the polypeptide set forth in SEQ ID NO:764, said isolated polypeptide comprising an amino acid sequence having at least 60 percent sequence identity with SEQ ID NO: 764.

198. An isolated polypeptide that is immunologically crossreactive with the polypeptide set forth in SEQ ID NO:764, said isolated polypeptide comprising an amino acid sequence having at least 60 percent sequence identity with SEQ ID NO: 764.

199. An isolated polypeptide comprising at least one epitope recognized by a T cell receptor specific for the polypeptide set forth in SEQ ID NO:764, wherein said isolated polypeptide comprises at least 10 amino acid residues and is encoded by a nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleotide sequence encoding SEQ ID NO:764.

200. An isolated polypeptide comprising at least one antigenic determinant of the polypeptide set forth in SEQ ID NO:764, wherein said isolated polypeptide comprises at least 10 amino acid residues and is encoded by a nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleotide sequence encoding SEQ ID NO:764.

201. An isolated polypeptide that is immunologically crossreactive with the polypeptide set forth in SEQ ID NO:764, wherein said isolated polypeptide comprises at least 10 amino acid residues and is encoded by a nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleotide sequence encoding SEQ ID NO:764.

202. An isolated polypeptide comprising at least 10 consecutive amino acid residues of SEQ ID NO: 764, wherein said polypeptide comprises at least one epitope recognized by a T cell receptor specific for the polypeptide set forth in SEQ ID NO:764.

203. An isolated polypeptide comprising at least 10 consecutive amino acid residues of SEQ ID NO: 764, wherein said polypeptide comprises at least one antigenic determinant of the polypeptide set forth in SEQ ID NO:764.

204. An isolated polypeptide comprising at least 10 consecutive amino acid residues of SEQ ID NO: 764, wherein said polypeptide is immunologically crossreactive with the polypeptide set forth in SEQ ID NO:764.

205. The isolated polypeptide of any one of claims 113 or 196-198 wherein said sequence identity with SEQ ID NO:764 is determined by

(1) aligning the amino acid sequence with SEQ ID NO:764 to identify the number of matching positions shared by the amino acid sequence and SEQ ID NO:764,

(2) dividing the number of matching positions by the total number of amino acids in SEQ ID NO:764, and

(3) multiplying the dividend by 100.

206. The isolated polypeptide of any one of claims 113 or 196-198 comprising at least 10 amino acid residues.

207. The isolated polypeptide of any one of claims 113, 120 or 196-201 comprising at least about 12 amino acid residues.

208. The isolated polypeptide of any one of claims 113, 120 or 196-201 comprising at least about 16 amino acid residues.

209. The isolated polypeptide of any one of claims 113, 120 or 196-201 comprising at least about 20 amino acid residues.

210. The isolated polypeptide of any one of claims 113, 120 or 196-201 comprising at least about 50 amino acid residues.

211. The isolated polypeptide of any one of claims 113, 120 or 196-201 comprising at least about 100 amino acid residues.

212. A composition comprising a fusion protein of claim 132 and a pharmaceutically acceptable carrier.

213. A composition comprising a fusion protein of claim 134 and a pharmaceutically acceptable carrier.

214. The isolated polypeptide of any one of claims 196-198 comprising an amino acid sequence having at least 70 percent sequence identity with SEQ ID NO: 764.

215. The isolated polypeptide of any one of claims 196-198 comprising an amino acid sequence having at least 80 percent sequence identity with SEQ ID NO: 764.

216. The isolated polypeptide of any one of claims 196-198 comprising an amino acid sequence having at least 90 percent sequence identity with SEQ ID NO: 764.

217. The isolated polypeptide of any one of claims 196-198 comprising an amino acid sequence having at least 95 percent sequence identity with SEQ ID NO: 764.

218. The isolated polypeptide of any one of claims 196-198 comprising an amino acid sequence having at least 98 percent sequence identity with SEQ ID NO: 764.

219. The isolated polypeptide of any one of claims 196-198 comprising an amino acid sequence having at least 99 percent sequence identity with SEQ ID NO: 764.

220. The isolated polypeptide of any one of claims 202-204 comprising at least about 12 consecutive amino acid residues of SEQ ID NO: 764.

221. The isolated polypeptide of any one of claims 202-204 comprising at least about 16 consecutive amino acid residues of SEQ ID NO: 764.

222. The isolated polypeptide of any one of claims 202-204 comprising at least about 20 consecutive amino acid residues of SEQ ID NO: 764.

223. The isolated polypeptide of any one of claims 202-204 comprising at least about 50 consecutive amino acid residues of SEQ ID NO: 764.

224. The isolated polypeptide of any one of claims 202-204 comprising at least about 100 consecutive amino acid residues of SEQ ID NO: 764.